An exclusively mesodermal origin of fin mesenchyme demonstrates that zebrafish trunk neural crest does not generate ectomesenchyme

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SUMMARY
The neural crest is a multipotent stem cell population that arises from the dorsal aspect of the neural tube and generates both non-ectomesenchymal (melanocytes, peripheral nerves and glia) and ectomesenchymal (skeletogenic, odontogenic, cartilaginous and connective tissue) derivatives. In amniotes, only cranial neural crest generates both classes, with trunk neural crest restricted to non-ectomesenchyme. In contrast, it has been suggested that anamniotes might generate derivatives of both classes at all axial levels, with trunk neural crest generating fin osteoblasts, scale mineral-forming cells and connective tissue cells; however, this has not been fully tested. The cause and evolutionary significance of this cranial/trunk dichotomy, and its absence in anamniotes, are debated. Recent experiments have disputed the contribution of fish trunk neural crest to fin osteoblasts and scale mineral-forming cells. This prompted us to test the contribution of anamniote trunk neural crest to fin connective tissue cells. Using genetics-based lineage tracing in zebrafish, we find that these fin mesenchyme cells derive entirely from the mesoderm and that neural crest makes no contribution. Furthermore, contrary to previous suggestions, larval fin mesenchyme cells do not generate the skeletogenic cells of the adult fin, but persist to form fibroblasts associated with adult fin rays. Our data demonstrate that zebrafish trunk neural crest does not generate ectomesenchymal derivatives and challenge long-held ideas about trunk neural crest fate. These findings have important implications for the ontogeny and evolution of the neural crest.

KEY WORDS: Fin mesenchyme, Dermomyotome, Ectomesenchyme, Fibroblast, Neural crest

INTRODUCTION
The neural crest is a multipotent embryonic stem cell population formed during neurulation from which numerous cell types derive, including pigment cells and neurons and glia of the peripheral nervous system (Le Douarin and Kalcheim, 1999). Pioneering histological (Landacre, 1921; Platt, 1893), xenotransplantation (Raven, 1932), quail-chick chimera (Le Lièvre and Le Douarin, 1975), cell labelling (Chibon, 1967; Horstadius and Sellman, 1946; Johnston, 1966) and cell extirpation (Stone, 1926; Stone, 1929) experiments have provided considerable evidence that, in addition to melanocytes and cells of the peripheral nervous system, anterior dorsal neural folds form cranial ectomesenchyme during neurulation. From this population arise skeletogenic, odontogenic and connective tissues of the craniofacial skeleton (reviewed by Le Douarin and Kalcheim, 1999). Despite the long history of neural crest research and the wealth of resulting information, many aspects of neural crest biology remain obscure or contentious. In particular, the precise lineage restriction of neural crest and the extent of its potency are debated.

In amniotes, the cranial neural folds are a major source of cartilage, skeletal and connective tissues of the head, whereas there appears to be no contribution of trunk neural crest to these tissues types of the body. How this dichotomy between trunk and cranial neural crest contributions arose during evolution is unclear. Hypotheses include a trunk environment not permissive for ectomesenchyme (McGonnell and Graham, 2002) and a topologically distinct (and cranial specific) source of ectomesenchyme within the neural ectoderm (Breau et al., 2008; Weston et al., 2004). In fish and amphibia, however, there have been a number of studies proposing that larval fin mesenchyme cells derive from trunk ectomesenchymal neural crest (reviewed by Hall and Hörstadius, 1988; Le Douarin, 1982; Le Douarin and Kalcheim, 1999). This was first suggested in the 1930s based on xenotransplantation and cell staining experiments (Detwiler, 1937; Holtfreter, 1935; Raven, 1936; Raven, 1932). This cell type was assumed to contribute to the connective tissue of the fins and thus to represent an ectomesenchyme derivative. In line with this, we recently described a role for larval fin mesenchyme cells in maturation of fin extracellular matrix (ECM) (Asharani et al., 2012).

The topic was largely neglected for decades until the advent of fluorescent vital dyes permitted cell fate analyses. Fluorescent labelling of Xenopus and zebrafish neural tissue supported a contribution of neural crest to larval fin mesenchyme (Collazo et al., 1993; Krotoski et al., 1988; Smith et al., 1994). However, in many of these experiments it was noted that tissue labelling was not always precise, and definitive characterisation of the derivative cells was not possible. Indeed, further vital dye labelling experiments identified an additional mesodermal contribution to fin mesenchyme cells of both the ventral (Tucker and Slack, 2004) and dorsal (Garriock and Krieg, 2007) larval fins, which has been confirmed by transplantation experiments in axolotls (Sobkow et al., 2006). Crucially, the relative contribution of the neural crest and mesoderm to fin mesenchyme cells has never been determined.
In addition to larval fin mesenchyme cells, trunk neural crest of teleosts had also been assumed to generate other ectomesenchymal derivatives, namely components of the adult post-cranial exoskeleton, which include the bony fin rays (lepidodotrichia) and scales (Sire and Akinmenko, 2004; Smith et al., 1994; Smith and Hall, 1990). Such assumptions were based on the fact that some intersegmental skeletal elements were believed to comprise odontogenic tissues and/or dermal bone. In mammals, these tissue types were long assumed to be generated exclusively from the cranial ectomesenchymal neural crest. For example, in evolutionary terms, the first mineralised tissue to arise in vertebrates is considered to be the mineralised body armour (Abzhanov et al., 2003; Lumsden, 1988; McGonnell and Graham, 2002). Evidence for the existence of trunk ectomesenchyme thus has important implications for understanding the evolution of skeletogenesis. However, more recent identification of an additional mesodermal contribution to the dermal bones of the cranial vault (reviewed by Gross and Hanken, 2008) suggested that dermal bones of the fins might not necessarily derive exclusively from neural crest. We have recently provided the first evidence of a neural crest origin of post-cranial dermal bone and scales in fish, and found that fin osteoblasts and scale mineral-forming cells, previously considered to be a trunk ectomesenchymal neural crest derivative, are in fact generated by paraxial mesoderm, with no discernible contribution from neural crest (Lee et al., 2013) (see also Mongera and Nüsslein-Volhard, 2013; Shimada et al., 2013). This surprising result led us to question the extent to which trunk neural crest generates larval fin mesenchyme, the only other described ectomesenchymal neural crest derivative of the trunk.

Through marker analysis, genetic ablation, transgenic labelling and time-lapse approaches we demonstrate that, as with fin osteoblasts, the mesenchyme of both the dorsal and ventral larval fins derives almost exclusively from the dermomyotome compartment of the paraxial mesoderm, whereas neural crest does not contribute. Further, we show that larval fin mesenchyme cells are retained into the adult fin where they become fin fibroblasts. Our data demonstrate that the trunk neural crest of zebrafish does not contribute any ectomesenchymal derivatives and suggest that amniotic trunk neural crest possesses the same diversity of fates as the trunk neural crest of amniotes.

**MATERIALS AND METHODS**

**Fish husbandry and lines**

Fish were maintained in the IMCB zebrafish facility and embryos were obtained through natural crosses and staged according to Kimmel et al. (Kimmel et al., 1995). nos jm; mob jm larvae were generated as described (Wang et al., 2011); the generation of the ET37 and ET5 lines is outlined by Parmigiani et al. (Parmigiani et al., 2004). For lineage analyses we used the previously described transgenic lines Tg(UAS:Kaedeg/Cry1)[Hatta et al., 2006], the wubi; switch Cre recombinase reporter line Tg(3.5Sub:loxP-eGFP-loxP-mCherry)cr1[Mosimann et al., 2011], the α-actin Gal4 line Tg(actc1b:Gal4)2781 [Maurya et al., 2011], the Sox10 eGFP line Tg(4.9sox10:eGFP)ba2[Carney et al., 2006] and the Pax3a eGFP line TgBAC(pax3a-eGFP)[Seger et al., 2011].

**In situ hybridisation and immunostaining**

Whole-mount embryo RNA in situ hybridisation was performed as described (Thiess and Thiess, 2008), developed with NBT/BCIP (Roche) and cleared in glycerol prior to imaging. Probes used were hnsn2 (Asharani et al., 2012), hnsn2 (Carney et al., 2010) and hbsn1 (Feitosa et al., 2012). Whole-mount embryo fluorescent immunostaining was performed as described (Asharani et al., 2012). Primary antibodies were: rat anti-eGFP (1:250; 04404-26, Nacalai Tesque), chicken anti-eGFP (1:500; ab13970, Abcam), rabbit anti-Kaede (1:250; PM012, MBL International), rabbit anti-DbRed/mCherry (1:250; 632496, BD Biosciences), mouse anti-Pax3/7 (1:200; DP312 [Davis et al., 2001]) and mouse zn5-5 (1:200; Zebrafish International Resource Center). Primary antibodies were detected using fluorescently conjugated secondary antibodies (1:400). Secondary antibodies were raised in donkey and were purchased from Jackson ImmunoResearch (Dylight 488 anti-chicken, Dylight 649 anti-rat) or Invitrogen (Alexa 546 anti-rabbit, Alexa 488 anti-rabbit, Alexa 647 anti-mouse, Alexa 546 anti-mouse).

**Sectioning, microscopy and photoconversion**

For transverse sections, embryo steaks were cut after in situ hybridisation or immunostaining using scalpel blades. Alternatively, cryosectioning was performed on embryos or adult fins using a Leica CM1900 cryostat, and the 16 μm sections then fluorescently immunostained. Confocal images and time-lapse movies were taken on an inverted Zeiss LSM700 or an upright Olympus BX61 Fluoview microscope, and high-magnification brightfield or Nomarski images were taken on a Zeiss AxioImager M2. For low-magnification brightfield images a Leica MZ16F stereo microscope was used. For time-lapse recordings of caudal fin development, anaesthetised embryos were mounted in 1% low melting point agarose (MO BIO Laboratories) in glass-bottom imaging dishes (MatTek) supplemented with 0.02% triazine (buffered to pH 7.0). Once solidified, the agarose was evacuated from around the tail of the embryos to permit normal tail morphogenesis, and the embryo overlaid with 0.5× E2 medium (7.5 mM NaCl, 0.25 mM KCl, 0.5 mM MgSO4, 75 μM KH2PO4, 25 μM NaHPO4, 0.5 mM CaCl2, 0.35 mM NaHCO3) containing 0.02% buffered triazine.

To follow Kaede-expressing cells by photoconversion, 24-hpf Kaede-positive embryos were mounted in agarose and imaged by confocal microscopy. A selected region of interest was converted using 60-80 pulses of 405 nm wavelength UV laser illumination. Embryos were then re-imaged immediately before being rescued from the agarose, and then re-examined 1 day later at 48 hpf.

**Tamoxifen treatment**

To induce Cre activity at specific time points in CreER2 transgenic embryos, 4-hydroxytamoxifen (Sigma) was dissolved in ethanol and added to dechorionated embryos in embryo medium at a final concentration of 5 μM as described (Mosimann et al., 2011). After exposure, the embryo medium was replaced and embryos were allowed to develop and then assessed for mCherry expression.

**PCR, transgene construct cloning, BAC recombineering and RNA synthesis**

PCR amplification was performed using PrimeStar (Takara Bio) on a DNA Engine thermocycler (BioRad). A 2.1 kb promoter region of ntlα was amplified by PCR from genomic DNA and cloned into the pSE-MCS vector (Kwan et al., 2007) by restriction digestion and ligation to generate pSE-2.ntlα. The 7.2 kb sox10 promoter (Promoter, 2008) and the 1.7 kb tbx6 promoter (Szeto and Kimelman, 2004) were transferred from standard vectors to pSE-MCS by restriction digestion and ligation. All transgene constructs were generated using multisite Gateway cloning methodology through the zebrafish Tol2kit (Kwan et al., 2007). Middle entry vectors containing lyn-tTomato, Gal4VP16, Cre and CreER2 were used in LR Clonase II Plus (Invitrogen) based recombination reactions. Reactions were conducted with Tol2-containing destination vectors, with or without the cmlc2:eGFP transgenesis marker where required.

The hncn2.CreER2[BAC] was generated by recombining a CreER2 cassette flanked by 60 bp arms homologous to the region around the translation start of the hncn2 gene. Recombination was performed using
RedET methodology (GeneBridges). A second recombination was performed targeting a Tol2-containing cassette (Suster et al., 2009) to the BAC vector, thus allowing improved efficiency of transgenesis.

Tol2 RNA was synthesised from Smal-linearised plasmid template and transcription performed with T3 RNA polymerase (Ambion).

Embryo injection and transgenesis
Plasmid DNA was prepared using the HiSpeed Plasmid Midi Kit (Qiagen) and BAC DNA using NucleoBond BAC 100 (Machery-Nagel). Embryos were injected with 30 ng/μl plasmid DNA and 30 ng/μl Tol2 RNA diluted in Phenol Red and Danieau’s buffer using a PLI-100 microinjector (Harvard Apparatus).

RESULTS
Substantial mesodermal contribution to larval fin mesenchyme
We have recently identified that in situ probes detecting bmp1a (Asharani et al., 2012), hemicentin 2 (hmcn2) (Carney et al., 2010) and fibulin 1 (fbln1) (Feitosa et al., 2012) mark fin mesenchyme cells from 48 hpf onwards (Fig. 1G,J,M). In addition, these cells are labelled by the enhancer trap lines ET37 and ET5 (Parinov et al., 2004), which also express eGFP in the apical ridge of the fins (Fig. 1A,D). Preceding this fin mesenchyme expression, all these markers shared a somitic expression domain, rather than neural crest expression, although ET5 was somewhat broader (Fig. 1B,C,E,F,H,I,K,L,N,O). This was surprising given the previous reports of at least a partial neural crest contribution to fin mesenchyme, and led us to investigate the source of these cells.

Expression domains can be dynamic, and it is possible that the somitic expression is not temporally contiguous with fin mesenchyme expression. To test this, we used time-lapse microscopy of the ET37 line to visualise the source of fin mesenchyme cells and noted that expression of eGFP was not biphasic, but continuous from the somitic expression through to fin mesenchyme cells (supplementary material Movies 1 and 2). We were able to track individual cells emigrating from both the ventral (Fig. 2A; supplementary material Movie 1) and dorsal (Fig. 2B; supplementary material Movie 2) somites into the fins where they became fin mesenchyme cells. To confirm that we were not tracking ectopically labelled neural crest cells, we generated a transgenic line that labels mesoderm with lyn-tdToma using the ntlα promoter (ntlα:lyn-tdtoma) (Harvey et al., 2010). At 24 hpf in the ventral fin, tdtama-positive cells could be seen as epithelial cells within somitic regions (Fig. 2C, left panel), a location and morphology inconsistent with neural crest cells. Time-lapse analysis of this line in the ET37 background confirmed that the eGFP-positive fin mesenchyme cells were derived from these ntlα-expressing epithelial mesodermal cells (Fig. 2C; supplementary material Movie 3).

To determine whether the contribution of the mesoderm was more extensive, we generated two lines expressing Gal4 in paraxial mesoderm using either the ntlα promoter or the tbx6 promoter (Szeto and Kimelman, 2004), and crossed them to the uas:kaedeE8 transgenic line (Hatta et al., 2006). In both lines, we noted strong paraxial mesodermal Kaede fluorescence at 24 hpf (Fig. 3A,D; data not shown), with the tbx6 promoter exhibiting a slightly more restricted expression pattern. Kaede protein was then photoconverted by UV laser at 24 hpf in either broad ventral or dorsal regions of the tail mesoderm (Fig. 3B,B′,E,E′). Imaging these embryos the following day revealed extensive labelling of mesodermal derivatives within the converted region, including muscle fibres as well as a large number of mesenchyme cells in the adjacent fin (Fig. 3C,C′,F,F′). This is consistent with our time-lapse data in demonstrating that fin mesenchyme derives from directly adjacent somitic domains.

Neural crest does not generate fin mesenchyme
Our data demonstrate that in zebrafish at least a significant proportion of both the dorsal and ventral fin mesenchyme cells are derived from the mesoderm. Recent literature has suggested that in amphibia the fin mesenchyme cells have a dual origin, deriving from both mesoderm and neural crest (Garriock and Krieg, 2007; Sobotkow et al., 2006; Tucker and Slack, 2004). We quantified the extent of neural crest labelling, we counted the number of Kaede-positive melanophores at 30 hpf, and noted that...
at least 93% (507/545 in five embryos) of melanophores examined were Kaede positive. We observed a limited number of Kaede-positive cells in the posterior fin (Fig. 4B,B'); however, crossing these double transgenics onto the ET37 background and immunostaining for eGFP and Kaede demonstrated that Kaede-positive neural crest cells never co-expressed eGFP (0/12 embryos analysed; Fig. 4C-C'), and thus cells of the fins that were derived from sox10-expressing neural crest do not appear to be fin mesenchyme cells. Indeed, upon imaging these cells under transmitted or incident light, we noted that in most cases the Kaede-positive cells displayed clear characteristics of pigment cells, either black melanophores (supplementary material Fig. S2A-B'), blue/yellowish xanthophores (supplementary material Fig. S2B-C') or iridescent iridophores (supplementary material Fig. S2C-C'). Occasionally Kaede-positive cells were seen in the fin that had no discernible pigmentation yet had a morphology inconsistent with fin mesenchyme and were never eGFP positive in the ET37 line. The identity of these cells is unknown but they might represent immature pigment cells. We conclude that, although neural crest cells do invade the zebrafish fin, they mostly generate pigment cells and do not appear to contribute to fin mesenchyme.

As an independent confirmation of our Kaede result, we generated a transgenic line expressing Cre recombinase under the sox10 promoter and crossed this to the ubi:switch reporter line (Mosimann et al., 2011), thus permanently labelling sox10-expressing cells with mCherry. The neural crest is labelled robustly and broadly at all axial levels (Lee et al., 2013). Imaging these embryos at 72 hpf demonstrated again that, whereas neural crest derivatives were mCherry positive, there were no mCherry-positive fin mesenchyme cells (supplementary material Fig. S3A-A').

We complemented these cell labelling data with an analysis of zebrafish embryos in which the neural crest had been genetically ablated. Zebrafish embryos doubly deficient for both tfap2a (mont blanc, motm616A) and foxd3 (mother superior, mosm188) (mob;mos embryos) have been shown to lack neural crest induction and are devoid of almost all neural crest derivatives (Wang et al., 2011). (Fig. 4D,E). If there is a neural crest contribution to fin mesenchyme, we might expect a reduction in the number of fin mesenchyme cells in mob;mos embryos. These embryos fully retained their medial fins, within which statistically indistinguishable numbers of fin mesenchyme cells were observed in both the wild-type and mos;mob embryos (Fig. 4F-H). It remains possible that loss of neural crest-derived fin mesenchyme could be obscured in this experiment through compensation from the mesoderm. However, in light of the genetic labelling experiments described above, we interpret the lack of any measurable fin mesenchyme reduction upon neural crest ablation as indicating no, or extremely limited, neural crest contribution.

**Paraxial mesoderm is the source of all fin mesenchyme**

We have provided evidence that both dorsal and ventral fin mesenchyme derives, at least partially, from paraxial mesoderm and not from neural crest. We next sought to determine whether the mesodermal contribution could account for all fin mesenchyme cells. We noted during our analysis of the tbx6:gal4; uas:kaede and the ntlagal4; uas:kaede embryos there was strong perdurance of Kaede protein to 48 hpf within fin mesenchyme and that in both lines the majority of fin mesenchyme cells were Kaede positive (Fig. 5A; data not shown). Neither migratory neural crest nor its derivatives were labelled by Kaede at 24 hpf (supplementary material Fig. S4A-A') or 48 hpf (data not shown). Crossing the ntlagal4; uas:kaede line to ET37 demonstrated that all fin mesenchyme cells labelled by eGFP are also Kaede positive (Fig. 5B-B'). This co-expression could be due to de novo expression from the ntlatal line within the fin mesenchyme cells at 48 hpf or represent perdurance from earlier promoter activity within the mesoderm. The former is unlikely as in situ hybridisation fails to detect ntlatal transcripts in fin mesenchyme cells at 48 hpf (data not shown) and our time-lapse analysis of the ntlatal-ltdtomato transgenics (Fig. 1C; supplementary material Movie 3) revealed rapid and permanent loss of tdTomato fluorescence in fin mesenchyme cells after immigration into the fin. To demonstrate
that the expression in the fin mesenchyme represents perdurance from earlier mesodermal expression, we photoconverted the Kaede in the tail of 
tla:gal4; uas:kaede transgenics at 24 hpf (supplementary material Fig. S5A-B'). Twenty-four hours later we observed almost complete expression of converted Kaede in the fin mesenchyme (supplementary material Fig. S5C,C'), demonstrating that the expression of Kaede in fin mesenchyme derives from the earlier somitic expression.

In addition, we used the Cre-Lox system as an independent lineage labelling method to confirm this result. 
tbx6:Cre; ubi:switch double-transgenic embryos showed induction of mCherry within the 
tbx6 expression domain and, later, broad mCherry expression within the fin mesenchyme domain (supplementary material Fig. S3B,B'). Thus, using two independent cell lineage tracing systems driven by two different promoters, we have demonstrated that fin mesenchyme cells are generated entirely from mesoderm and are not neural crest derived.

**Fin mesenchyme is a dermomyotome derivative**

To delineate the somitic compartment from which fin mesenchyme is derived, we labelled the myotome using the α-actin transgenic line 
Tg(actc1b:Gal4i269) (Maurya et al., 2011) and the sclerotome with a transgenic line, Tg(Ola-Twist:Gal4), in which the medaka Twist promoter (Inohaya et al., 2007) drives Gal4. Crossing both of these to the uas:kaede line allowed us to trace derivatives of the myotome and sclerotome. Despite observing cells in the expected locations at 24 hpf and 48 hpf (supplementary material Fig. S4B-B'; data not shown), we did not observe Kaede fluorescence in the fin mesenchyme in either case (Fig. 5C-D'). Lack of myotome or sclerotome contribution to fin mesenchyme indicated they were likely to be derived from the dermomyotome compartment. Indeed, when we analysed the TgBAC(pan3a:eGFP) transgenic line (Seger et al., 2011), which reproduces the expression of Pax3 in the dermomyotome (see also supplementary material Fig. S4C-C'), we noted expression of eGFP in almost all fin mesenchyme cells at 48 hpf (Fig. 5E,E'). To confirm that this is not de novo expression in the fin mesenchyme and represents perdurance of eGFP from the dermomyotome at 24 hpf, we performed time-lapse microscopy and observed eGFP-positive fin mesenchyme cells emerging from the somites and invading the fin (two dermomyotome cells are tracked in Fig. 5F; supplementary material Movie 4). Additionally, the neural crest is strongly labelled in this line. Although neural crest cells also invaded the fins they were clearly discernible from fin mesenchyme cells based on their size, eGFP intensity and migratory behaviour.

We conclude that fin mesenchyme cells are dermomyotome derivatives and that, coupled with their morphology, expression of ECM molecules and modifying enzymes as well as a described role in ECM remodelling, they can be considered fibroblasts.

**Fin mesenchyme cells persist in the fins into adulthood as fibroblasts**

We have recently shown that lepidotrichial skeletogenic cells invade the adult fin between 2 and 3 weeks of age, and do not arise from cells present in the larval fin fold at 5 dpf (Lee et al., 2013). If fin mesenchyme cells do not generate the osteoblasts of the fin
rays, we questioned whether they contribute to any of the cells of the adult fin or are lost during juvenile stages of development. To address this, we conducted time point analysis of \textit{tbx6:CreERt2; ubi:switch} transgenics. Embryos were treated with 4-hydroxytamoxifen from 8 hpf to 48 hpf to label cells of the paraxial mesoderm. As with the \textit{tbx6:Cre; ubi:switch} double transgenics, we observed fin mesenchyme cells in the fins of a number of individuals at 5 dpf (Fig. 6A). We followed these cells over subsequent days and noted that they remained within the fin until at least 21 dpf, when chains of cells were also observed (Fig. 6B).

To assess whether they persist into adult stages, we permanently and specifically labelled them by generating an \textit{hmcn2:CreERt2} transgene through BAC homologous recombination (see Materials and methods). This construct was injected into the \textit{ubi:switch} transgenic line and subsequently treated with 4-hydroxytamoxifen at 80-116 hpf. Three days later at 7 dpf, scattered mCherry-positive fin mesenchyme cells could be seen within the fin (Fig. 6C). Over subsequent days and noted that they remained within the fin until at least 21 dpf, when chains of cells were also observed (Fig. 6B).

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**DISCUSSION**

The emergence of neural crest was a pivotal moment in the evolution of vertebrates and has been proposed to have occurred at the anterior of a hypothetical protochordate during the generation of a ‘new head’ (Gans and Northcutt, 1983). Here, neural crest was proposed to take on many roles of the trunk mesoderm, generating head connective and skeletal tissues (ectomesenchyme). There has been considerable conjecture as to whether trunk neural crest also evolved to generate such ectomesenchymal derivatives. Evidence of a neural crest contribution to fin connective tissue in amphibians has been invoked as evidence in support of this. Indeed, we have demonstrated that fin mesenchyme does resemble and function as fibroblastic connective tissue cells. However, through transgenic cell lineage tracing and mutant analysis, we have shown that zebrafish fin mesenchyme is not a derivative of trunk neural crest but is entirely derived from paraxial mesoderm, specifically the dermomyotome. This, in combination with our previous result that mineralising cells of the adult fin rays and scales are not an ectomesenchymal
neural crest derivative (Lee et al., 2013), suggests that the trunk neural crest of zebrafish does not have ectomesenchymal fates, and thus resembles mammalian trunk neural crest in its repertoire of derivatives. This challenges long-held ideas about trunk neural crest lineages in anamniotes.

It should be noted that previous work has led to the belief that trunk neural crest in amphibia partially contributes (along with mesoderm) to fin mesenchyme. A single cell type originating from two distinct germ layers in a simple tissue such as the fin fold seems unusual, although a mixed origin is observed in more complex anatomical structures such as the calvaria (Gross and Hanken, 2008). While it is possible that the trunk neural crest of amphibia is unique in this regard and has acquired ectomesenchyme fates during evolution (or, conversely, mammals and teleosts have independently lost this lineage from trunk neural crest), in light of our data it would be worthwhile re-examining the fates of amphibian trunk neural crest more precisely. Our analysis indeed demonstrated the extremely close proximity of neural crest and dermomyotome during early development as well as a neural crest contribution of pigment cells to the fin. This challenges long-held ideas about trunk neural crest lineages in anamniotes.

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One implication of our findings concerns the existence and properties of neural crest cells in vivo. An extensive body of evidence has shown that pigment cells, peripheral neurons and glia share a common precursor with ectomesenchymal derivatives within cranial neural folds (Baroffio et al., 1991; Blentic et al., 2008; Chan and Tam, 1988; Essex et al., 1993; Osumi-Yamashita et al., 1994; Pohl and Knöchel, 2001). More recent experiments in the mouse mapped the cranial neural fold territory with greater spatial and temporal resolution, and led to the controversial proposal of a distinct origin (the metablast) for ectomesenchyme (Breau et al., 2008; Weston et al., 2004). Although this contentious notion is less well accepted, such a topological partitioning of ectomesenchyme and non-ectomesenchyme birth sites would be incompatible with the model of a homogeneous multipotent neural crest territory. In agreement with this segregation model was the observation that neural crest cells are fate restricted in the zebrafish head and trunk prior to delamination (Raible and Eisen, 1994; Schilling and Kimmel, 1994). Although our investigations do not address the question of the existence of a metablast directly, they do argue...
agains the existence of a neural crest stem cell in the trunk of fish that generates both neuronal/pigment and ectomesenchyme, which had previously been invoked as evidence for neural crest multipotency. It must be stressed that we have only interrogated the fates of trunk neural crest, which must be seen as distinct from questions of potency. Indeed, it has been reported that trunk neural crest cells are, under certain experimental conditions, able to generate bone, cartilage and dentine (Abzhanov et al., 2003; Lumsden, 1988; McGonnell and Graham, 2002). Our data argue that such permissive conditions do not exist in the tail/trunk of zebrafish. Conversely, we have demonstrated that the dermomyotome does respond to the fin environment, which promotes the immigration and differentiation of these cells into fibroblasts.

Little is known about the mechanisms controlling these events, and the zebrafish fin mesenchyme offers a tractable system with which to identify genetic and cellular systems controlling dermomyotome/fibroblast biology. Although our data demonstrate that these larval fin mesenchyme fibroblasts do not later contribute to the osteoblast lineage of the adult lepidotrichia (Lee et al., 2013), they do remain in the adult fins as fibroblasts. We suspect their function at this location is in modelling/repair of the ECM at these sites, in particular the actinotrichia of the distal adult lepidotrichia, mirroring their larval role. Indeed, during regeneration these cells have been observed to accumulate at the distal tip of the blastema (Nechiporuk and Keating, 2002; Poleo et al., 2001; Tu and Johnson, 2011), where actinotrichia form to guide regrowing lepidotrichia (Asharani et al., 2012; Durán et al., 2011). The regenerative plasticity of these fibroblasts within this distal blastema has been of interest to the fin regeneration field for a number of years; however, a number of recent reports indicate that fibroblasts do not normally regenerate other lineages after fin amputation (Knopf et al., 2011; Sousa et al., 2011; Stewart and Stankunas, 2012; Tu and Johnson, 2011). Recently, it has been shown that upon disruption of normal osteoblast regeneration, these fibroblasts may exhibit a degree of plasticity to compensate (Singh et al., 2012). Using our ability to label intra-ray fibroblasts, it will be interesting to determine the extent of plasticity exhibited by these cells during normal or perturbed fin regeneration.

We have now tested all three purported ectomesenchyme derivatives of trunk neural crest and found in all cases that they are mesoderm derived. Thus, the trunk neural crest of zebrafish is restricted, as is that of amniotes, to non-ectomesenchymal derivatives. The ability of trunk neural crest to generate ectomesenchyme was considered to be a feature of early vertebrates and central to the formation of the first mineralised skeleton of the vertebrate subphylum, the dermal armour of stem gnathostomes. The zebrafish fin mesenchyme and post-cranial exoskeleton were assumed to represent a relic of this early trunk neural crest ectomesenchyme (Smith et al., 1994). Our data cast doubt on this hypothesis and on the generation of ectomesenchymal derivatives from trunk neural crest in both fish and amniotes. By showing that the trunk exoskeleton and connective tissue cells of the fins are derived from mesodermal mesenchyme, our findings raise the possibility that the first mineralised skeleton of vertebrates was in fact of mesodermal origin.

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Competing interests statement
The authors declare no competing financial interests.

Author contributions
R.T.H.L. and T.J.C. designed and performed experiments and wrote the paper. E.W.K. and J.P.T. provided reagents and edited the manuscript.

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Fig. S1. Neural crest cells are well labelled in *sox10:gal4; uas:kaede* embryos. Lateral confocal images of 30-hpf (A,C,C') and 48-hpf (B) *sox10:gal4; uas:kaede* transgenic embryos immunostained with an antibody detecting Kaede. (A) Broad and robust neural crest labelling along the entire axis can be seen at 30 hpf. (B) Lateral view of the branchial arches at 48 hpf showing extensive labelling of presumptive ectomesenchymal neural crest. (C,C') Images showing DIC alone (C) or overlaid on a fluorescent image of Kaede expression demonstrates labelling of melanophores in *sox10:gal4; uas:kaede* transgenic embryos (C'). In this image, it can be seen that all five melanocytes express Kaede. Quantification of five 30-hpf *sox10:gal4; uas:kaede* transgenic embryos showed that at least 93.0% of melanophores are labelled by Kaede (a total of 545 melanophores was counted).

Fig. S2. Kaede-positive cells in the fin are chromatophores. (A-C') Lateral views of the fin region of three 3-dpf *sox10:gal4; uas:kaede* transgenic embryos displaying Kaede green fluorescence (A,B,C) and brightfield views (A',B',C'). An overlay of the fluorescence image on the brightfield image is also shown (A'',B'',C''). At both low (A-A'') and high (B-C'') magnification, it can be observed that the Kaede-positive cells in the fin (A,B,C) correspond to black melanophores (m; A',A'',B',B'',C',C''), xanthophores with characteristic yellow/blue colouration (x; A',A'',B',B'',C',C'') or reflective iridophores (i; C',C'').
Fig. S3. Permanent lineage analysis confirms the origin of embryonic fin mesenchyme. (A,A') Lateral confocal images of 72-hpf sox10:Cre; ubi:switch embryos fluorescently immunostained with an antibody detecting mCherry. Image of mCherry expression within the posterior trunk and fin (A) and also superimposed on a Nomarski view to show limited cells within the fin (A'). These embryos have neural crest lineages permanently labelled with mCherry, and show labelled cells within the trunk in locations and with morphology consistent with described neural crest derivatives. Fin mesenchyme is unlabelled. (B,B') Lateral confocal images of 3-dpf tbx6:Cre; ubi:Switch embryos fluorescently immunostained with an antibody detecting mCherry. (B) mCherry expression within the posterior trunk and fin with widespread expression visible in the fin mesenchyme and muscle of trunk. (B') Fluorescent image superimposed on a Nomarski view outlining expression domains within the fin.
Fig. S4. Analysis of transgenic lines used to define the origin of fin mesenchyme. Transverse cryosections of the trunk region of the \textit{ntla:gal4; uas:kaede} (A-A’), the \textit{Ola-Twist:gal4; uas:kaede} (B-B’) and the \textit{TgBAC(pax3a:EGFP)i150} (C-C’) transgenic lines at 24 hpf, imaged by confocal microscopy following fluorescent immunostaining with antibodies against eGFP (A-A’), Kaede (A-A’, B-B’), and Pax3/7 (C-C’). All sections were counterstained with DAPI (blue). (A-A’) To demonstrate exclusion of Kaede expression from neural crest, the \textit{ntla:gal4; uas:kaede} line was crossed to the \textit{sox10:egfpba2} line and immunostained for eGFP (A) and Kaede (A’). Restriction of Kaede to the mesoderm and exclusion from the neural crest can be seen in the superimposed image (A”). (B-B’) Expression of Kaede in the \textit{Ola-Twist:gal4; uas:kaede} line is largely restricted to the sclerotomal compartment of the somites as seen by immunostaining for Kaede expression (B), which can be seen in a medial somitic location (B’) and far removed from the superficial dermomyotome domain. Occasional myotome expression can be observed in this line (B”). (C-C’) The \textit{TgBAC(pax3a:EGFP)i150} line faithfully recapitulates Pax3 expression in the dermomyotome as shown by comparing eGFP immunofluorescence (C) with Pax3/7 immunoreactivity (C’). By superimposition of the two confocal images, eGFP-positive dermomyotome cells at the somite surface have Pax3/7-positive nuclei, with strong eGFP and Pax3/7 colabelling in the dorsal neural tube and neural crest also apparent (C”).
**Fig. S5. Photoconversion of Kaede demonstrates that fin mesenchyme derives from earlier ntlA mesoderm expression domains.** (A–C') The tail region of an ntlA:gal4: uas:kaede transgenic embryo imaged at 24 hpf (A-B') and again at 48 hpf (C,C') both prior to (A,A') and after (B-C') Kaede photoconversion. Unconverted Kaede protein is shown in the green channel, which is overlaid with UV-photoconverted Kaede in the red channel (A,B,C). The red channel is additionally displayed alone for clarity (A',B',C'). The Kaede protein present at 48 hpf in the fin mesenchyme is photoconverted, demonstrating that it corresponds to perdurance of Kaede from the mesodermal expression domain at 24 hpf.

**Movie 1. Ventral fin mesenchyme cells emerge from ventral somites.** Confocal time-lapse movie of the tail region of an ET37 transgenic embryo imaged from 26 hpf for ~20 hours at 10-minute intervals. A fin mesenchyme cell is highlighted (arrow) leaving the ventral somite and taking up location in the ventral fin.
Movie 2. Dorsal fin mesenchyme cells emerge from dorsal somites. Confocal time-lapse movie of the tail region of an ET37 transgenic embryo imaged from 29 hpf for ~18 hours and 20 minutes at 8-minute intervals. A fin mesenchyme cell is highlighted (arrow) leaving the dorsal somite and taking up location in the dorsal fin.

Movie 3. Fin mesenchyme emerges from an ntl:lyn-tdtomato-expressing somitic domain. Confocal time-lapse movie of the tail region of an ntl:lyn-tdtomato ET37 transgenic embryo, imaged from 22 hpf for ~12 hours at 8-minute intervals. The ET37 eGFP signal is shown in green, with membrane-tethered tdTomato driven by the ntl promoter in magenta. The first frame omits the GFP signals to highlight the epithelial nature of the tdTomato-expressing cells. Two cells, initially epithelial and expressing tdTomato, are indicated by arrows and followed out into the fin where they rapidly lose tdTomato expression and gain strong eGFP expression.

Movie 4. Fin mesenchyme derives from the pax3a-expressing dermomyotome. Confocal time-lapse movie of the tail region of a TgBAC(pax3a:EGFP)i150 transgenic embryo, imaged from 24 hpf for ~16 hours at 8-minute intervals. This line labels the neural crest, the dorsal neural tube and the dermomyotome, the latter being distinguishable from the former two as it has a less intense GFP signal. Fin mesenchyme cells can be tracked from the somite into the fins (two examples are indicated by arrows). Neural crest cells also invade the fins but show both increased intensity of GFP and migratory behaviour in comparison to the fin mesenchyme cells.